

## EXHIBIT A

### Summary Of Nogo Hydrophilicity Analysis

<u>Tax No of Exhibit B</u>	<u>Amino Acid Sequence of Interest ("I")</u>	<u>Claim</u>	<u>Analyzed Amino Acid Sequence ("A")</u>	<u>Amino Acid positions of I in A</u>	<u>Point Of Greatest Local Hydrophilicity</u>
1	amino acids 1-171 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-171 in the blot corresponding to aa 1-171 of SEQ ID NO:2	ca. aa 42
2	amino acids 172-974 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-803 in the blot corresponding to aa 172-974 of SEQ ID NO:2	Peaks throughout the protein
3	amino acids 542-722 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-181 in the blot corresponding to aa 542-722 of SEQ ID NO:2	ca. aa 114
4	amino acids 172-723 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-552 in the blot corresponding to aa 172-723 of SEQ ID NO:2	ca. aa 145
5	amino acids 1-974 of SEQ ID NO:2	Claim 135	entire sequence of interest	aa 1-974 in the blot corresponding to aa 1-974 of SEQ ID NO:2	Peaks throughout the protein
6	amino acids 1-131 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-131 in the blot corresponding to aa 1-131 of SEQ ID NO:29	ca. aa 40

<u><b>Tax No of Exhibit B</b></u>	<u><b>Amino Acid Sequence of Interest ("I")</b></u>	<u><b>Claim</b></u>	<u><b>Analyzed Amino Acid Sequence ("A")</b></u>	<u><b>Amino Acid positions of I in A</b></u>	<u><b>Point Of Greatest Local Hydrophobicity</b></u>
7	amino acids 132-939 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-808 in the blot corresponding to aa 132-939 of SEQ ID NO:29	Peaks throughout the protein
8	amino acids 206-501 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-296 in the blot corresponding to aa 206-501 of SEQ ID NO:29	ca. aa 112
9	amino acids 501-680 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-180 in the blot corresponding to aa 501-680 of SEQ ID NO:29	ca. aa 162
10	amino acids 132-206 of SEQ ID NO:29	Claim 136 & 137	aa 100-300 of SEQ ID NO:29	aa 32-106 in the blot corresponding to aa 132-206 of SEQ ID NO:29	ca. aa 36
11	amino acids 680-939 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-260 in the blot corresponding to aa 680-939 of SEQ ID NO:29	Peaks throughout the protein
12	amino acids 940-1127 of SEQ ID NO:29	Claim 136 & 137	entire sequence of interest	aa 1-188 in the blot corresponding to aa 940-1127 of SEQ ID NO:29	ca. aa 23 and aa 32
13	amino acids 623-640 of SEQ ID NO:2	Claim 135	aa 550-750 of SEQ ID NO:2	aa 73-90 in the blot corresponding to aa 623-640 of SEQ ID NO:2	ca. 80

<u>Tax No of Exhibit B</u>	<u>Amino Acid Sequence of Interest ("I")</u>	<u>Claim</u>	<u>Analyzed Amino Acid Sequence ("A")</u>	<u>Amino Acid positions of I in A</u>	<u>Point Of Greatest Local Hydrophility</u>
14	SEQ ID NO:43	Claim 135	aa 1-200 of SEQ ID NO. 29	aa 1-13 in the blot corresponding to aa 1-13 of SEQ ID NO. 29	ca. 10
15	SEQ ID NO:44	Claim 135	aa 100-300 of SEQ ID NO. 29	aa 88-104 in the blot corresponding to aa 187-203 of SEQ ID NO. 29	ca. 95
16	SEQ ID NO:45	Claim 135	aa 250-450 of SEQ ID NO. 29	aa 91-111 in the blot corresponding to aa 570-619 of SEQ ID NO. 29	ca. 105
17	SEQ ID NO:46	Claim 135	entire sequence of interest	aa 1-50	21
18	Amino acids 762-1163 of SEQ ID NO:2	Claim 135	Entire sequence of interest	aa 1-402	ca. 195

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## ProtScale

User-provided sequence:

```
      1      11      21      31      41      51
      |      |      |      |      |      |
1 MEDIDQSSLV SSSTDSPRP PPAFKYQFVT EPEDEEDEEE EDEEEDDED LEELEVLERK 60
61 PAAGLSAAAV PPAAAPLLD FSSDSVPPAP RGPLPAAPPA APERQPSWER SPAAPAPSLP 120
121 PAAAVLPSKL PEDDEPPARP PPPPPAGASP LAEPAAPPST PAAPKRRGSG S
```

SEQUENCE LENGTH: 171

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

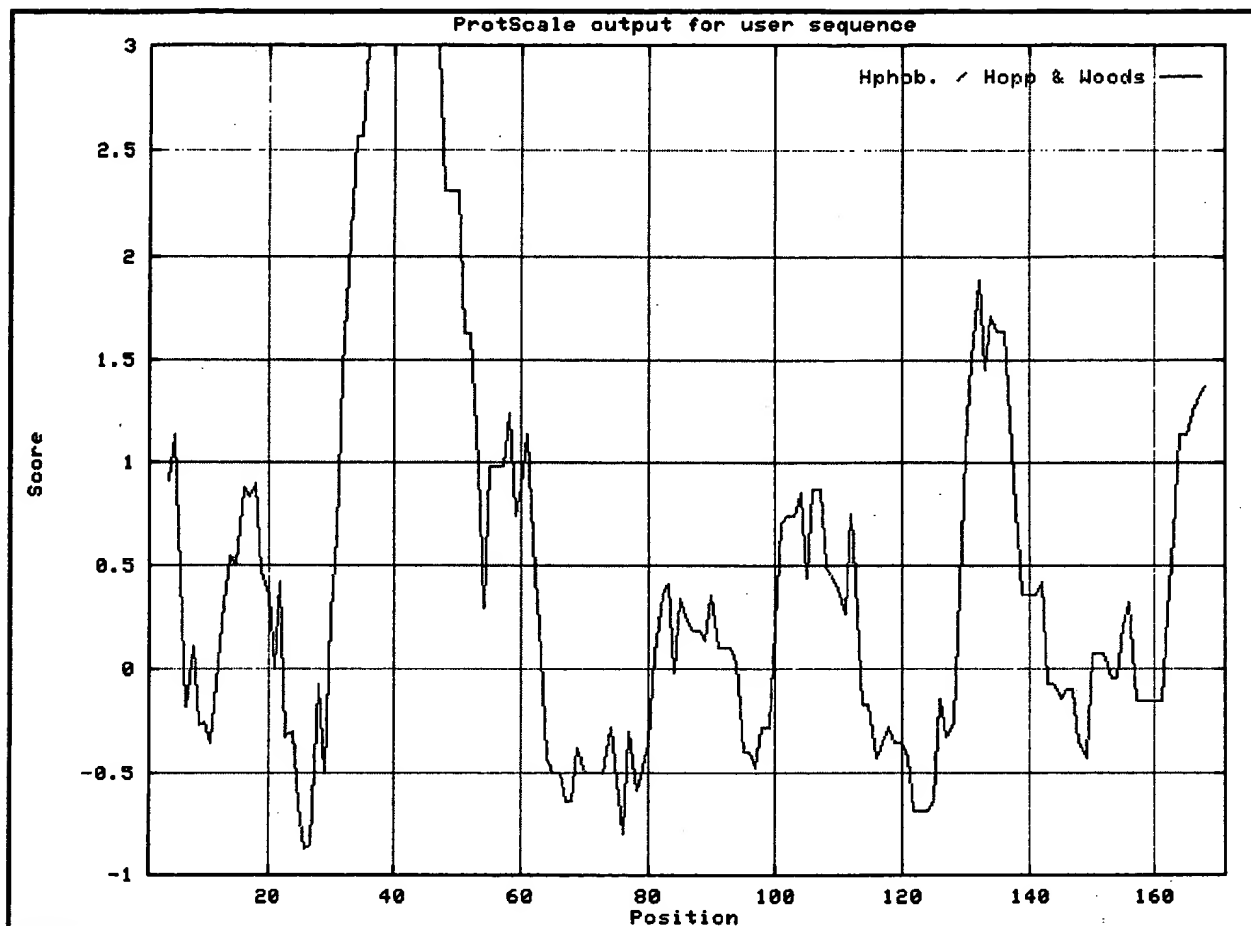
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -0.871

MAX: 3.000

1-171 of  
SEQ ID No 2  
(claim 13) (15)



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## ProtScale

User-provided sequence:

	1	11	21	31	41	51	
1	VDETLFALPA	ASEPVI	PSSA	EKIMDL	MEQP	GNTVSS	GQED FPSVLLETAA SLPSLSPLST 60
61	VSFKEHGYLG	NLSAVS	SSEG	TIEETL	NEAS	KELPER	ATNP FVNRDLAEFS ELEYSEMGS 120
121	FKGSPKGESA	ILVENT	KEEV	IVRSKD	KEDL	VCSAAL	HSPQ ESPVGKEDRV VSPEKTMDF 180
181	NEMQMSVVAP	VREEYA	DFKP	FEQAW	EVKDT	YEGSRD	VLAA RANVESKVDR KCLEDSLEQK 240
241	SLGKDSEGRN	EDASFP	STPE	PVKDSS	RAYI	TCASFT	SATE STTANTFPLL EDHTSENKTD 300
301	EKKIEERKAQ	IITEKT	SPKT	SNPFLV	AVQD	SEADYV	TTDT LSKVTEAAVS NMPEGLTPDL 360
361	VQEACESELN	EATGTK	IAYE	TKVDLV	QOTSE	AIQESL	YPTA QLCPSFEEAE ATPSPVLPDI 420
421	VMEAPLNLL	PSAGAS	VVQP	SVSPLE	APPP	VSYDSI	KLEP ENPPPYEEAM NVALKALGTK 480
481	EGIKEPESFN	AAVQET	EAPY	ISIACD	LIKE	TKLSTE	PSPD FSNYSEIAKF EKSVPHEAEL 540
541	VEDSSPESEP	VDLFSD	DSIP	EVPTQ	QEEAV	MLMKES	LTEV SETVAQHKEE RLSASPQELG 600
601	KPYLESFQPN	LHSTKD	AASN	DIPTLT	KKEK	ISLQME	EFTNT AIYSNDDLLS SKEDKIKESE 660
661	TFSDSSPIEI	IDEFPT	TVSA	KDDSPK	LAKE	YTDLEV	SDKS EIANIQSGAD SLPCLELPCD 720
721	LSFKNIYPKD	EVHVS	DEFSE	NRSSVS	KASI	SPSNVS	ALEP QTEMGSIKVS KSLTKEAEKK 780
781	LPSDTEKEDR	SLSAVL	SAEL	SKT			

SEQUENCE LENGTH: 803

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

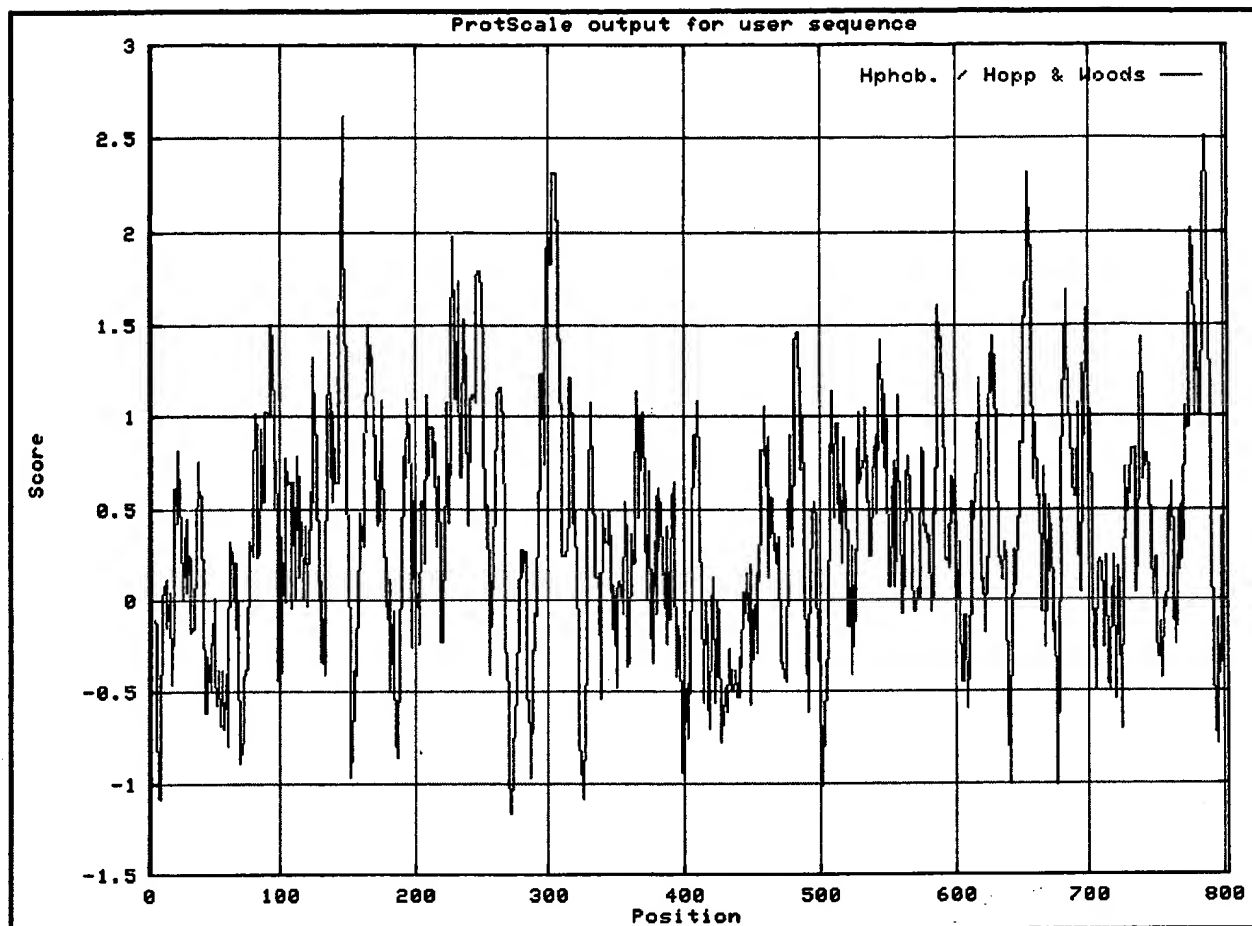
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171

MAX: 2.614

172-974 of  
SEADU6:2  
(chain 13) (16)



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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	EATGTKIAYE	TKVDLVQTSE	AIQESLYPTA	QLCPSFEEAE	ATPSPVLPDI	VMEAPLNSLL 60
61	PSAGASVVQP	SVSPLEAPP	VSYDSIKLEP	ENPPPYEEAM	NVALKALGTK	EGIKEPESFN 120
121	AAVQETEAPY	ISIACDLIKE	TKLSTEPSPD	FSNYSEIAKF	EKSVPEHAEL	VEDSSPESEP 180
181	V					

SEQUENCE LENGTH: 181

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,...,7, using **linear weight variation model**:

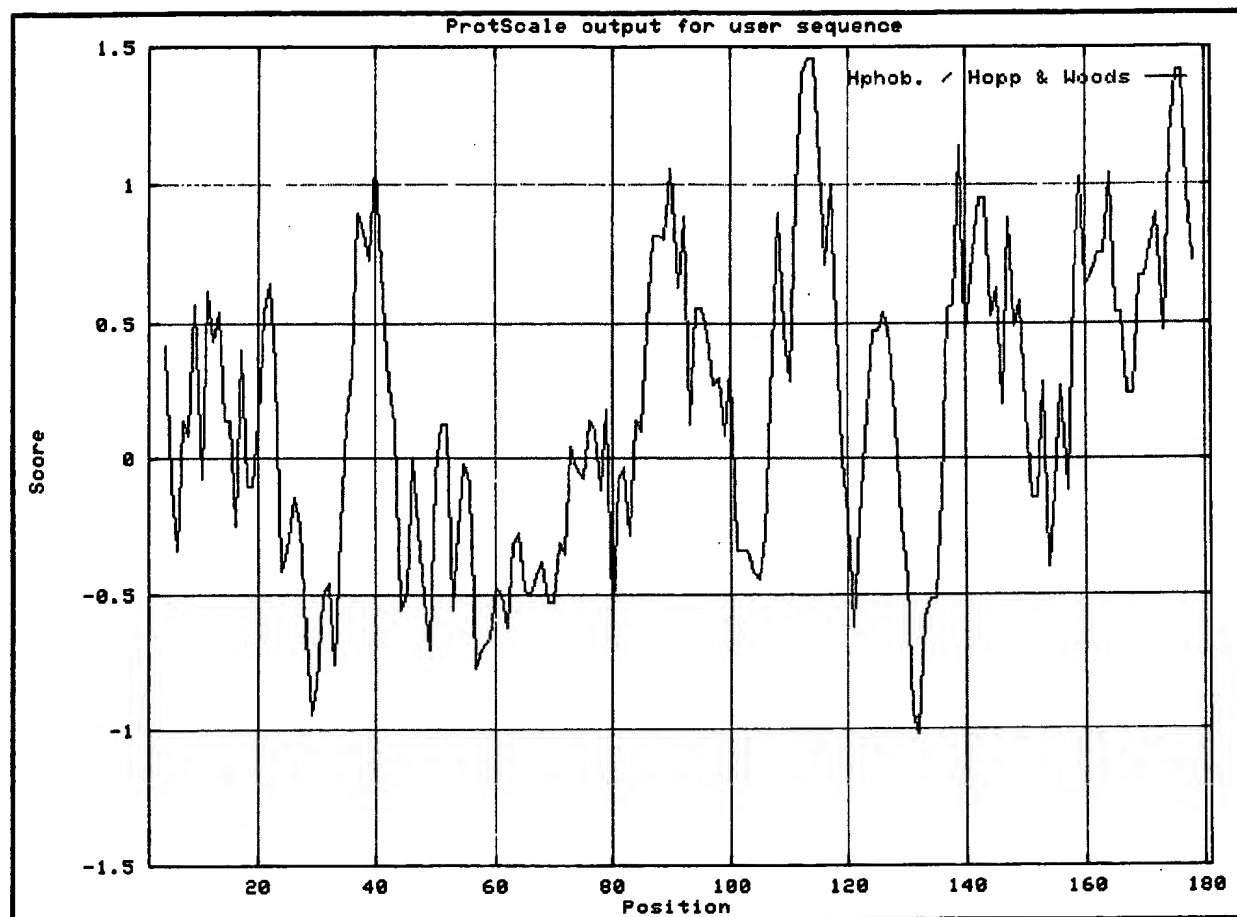
1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.014

MAX: 1.457

542-722 of  
SEQ ID No. 2  
(chain 13) 18





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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	VDETLFALPA	ASEPVI	PSSA	EKIMDL	MEQP	GNTVSSGQED FPSVLLETAA SLPSLSPLST 60
61	VSFKEHGYLG	NLSAVSS	SEG	TIEETL	NEAS	KELPERATNP FVNRDLAEFS ELEYSEMGSS 120
121	FKGSPKGESA	ILVENTKE	EV	IVRSKD	KEDL	VCSAALHSPQ ESPVGKEDRV VSPEKTMDIF 180
181	NEMQMSVVAP	VREEYADF	KP	FEQAW	EVKDT	YEGSRDVLAA RANVESKVDR KCLEDSLEQK 240
241	SLGKDSEGRN	EDASFP	STPE	PVKDSS	RAYI	TCASFTSATE STTANTFPLL EDHTSENKTD 300
301	EKKIEERKAQ	IITEKT	SPKT	SNPFL	VAVQD	SEADYVTTDT LSKVTEAAVS NMPEGLTPDL 360
361	VQEACESELN	EATGTK	IAYE	TKVDL	VQTSE	AIQESLYPTA QLCPSFEEAE ATPSPVLPDI 420
421	VMEAPLNSLL	PSAGAS	VVQP	SVSPLE	APP	VSYDSIKLEP ENPPPYEEAM NVALKALGTK 480
481	EGIKEPESFN	AAVQET	EAPY	ISIACD	LIKE	TKLSTEPSPD FSNYSEIAKF EKSVPHEAEL 540
541	VEDSSPESEP	VD				

SEQUENCE LENGTH: 552

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

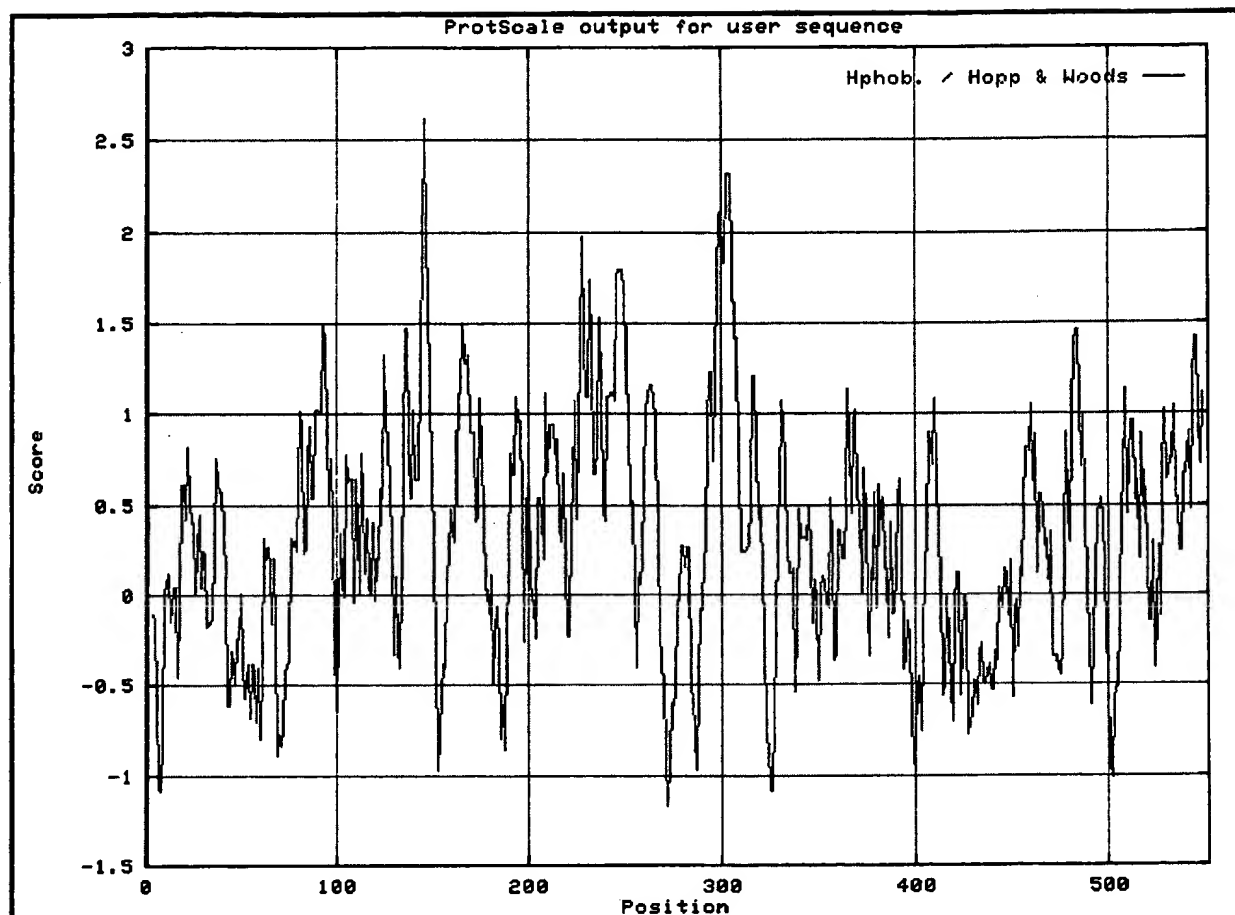
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171

MAX: 2.614

172-723 of  
SEQ ID NO. 2  
(claim 13) (21)



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# ProtScale

User-provided sequence:

	1	11	21	31	41	51	
1	MEDIDQSSLV	SSSTDSPPRP	PPAFKYQFVT	EPEDDEDEEE	EEDEEEDDED	LEELEVLERK	60
61	PAAGLSAAAV	PPAAAAPLLD	FSSDSVPPAP	RGPLPAAPPA	APERQPSWER	SPAAPAPSLP	120
121	PAAAVLPSKL	PEDDEPPARP	PPPPPAGASP	LAEPAAPST	PAAPKRRGSG	SVDETLFALP	180
181	AASEVPVPSS	AEKIMDLMEQ	PGNTVSSGQE	DFPSVLLETA	ASLPSLSPLS	TVSFKEHGYL	240
241	GNLSAVSSSE	GTIEETLNEA	SKELPERATN	PFVNRDLAEF	SELEYSEMGS	SFKGSPKGES	300
301	AILVENTKEE	VIVRSKDKED	LVCSAALHSP	QESPVGKEDR	VVSPEKTMDI	FNEMQMSVVA	360
361	PVREEYADFK	PFEQAWEVKD	TYEGSRDVLA	ARANVESKVD	RKCLEDSELEQ	KSLGKDSEGR	420
421	NEDASFPSTP	EPVKDSSRAY	ITCASFTSAT	ESTTANTFPL	LEDHTSENKT	DEKKIEERKA	480
481	QIITEKTSPK	TSNPFLVAVQ	DSEADYVTTD	TLISKVTEAAV	SNMPEGLTPD	LVQEACESEL	540
541	NEATGTKIAY	ETKVDLVQTS	EAIQESLYPT	AQLCPSFEEA	EATPSPVLDP	IVMEAPLNSL	600
601	LPSAGASVVQ	PSVSPLEAPP	PVSYSIKLE	PENPPPYEEA	MNVALKALGT	KEGIKEPESF	660
661	NAAVQETEAP	YISACDLIK	ETKLSTEPSP	DFSNYSEIAK	FEKSVPEHAE	LVEDSSPESE	720
721	PVDLFSDDSI	PEVPQTQEEA	VMLMKESLTE	VSETVAQHKE	ERLSASPQEL	GKPYLESFQP	780
781	NLHSTKDAAS	NDIPTLTKEE	KISLQMEEFN	TAIYSNDDLL	SSKEDKIKES	ETFSOSSPIE	840
841	IIDEFPTFVS	AKDDSPKLAK	EYTDLEVSDK	SEIANIQSGA	DSLPCLELPC	DLSFKNIYPK	900
901	DEVHVSDEFS	ENRSSVSKAS	ISPSNVSALE	PQTEMGSIKV	SKSLTKEAEK	KLPSDTEKED	960
961	RSLSAVLSAE	LSKT					

SEQUENCE LENGTH: 974

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

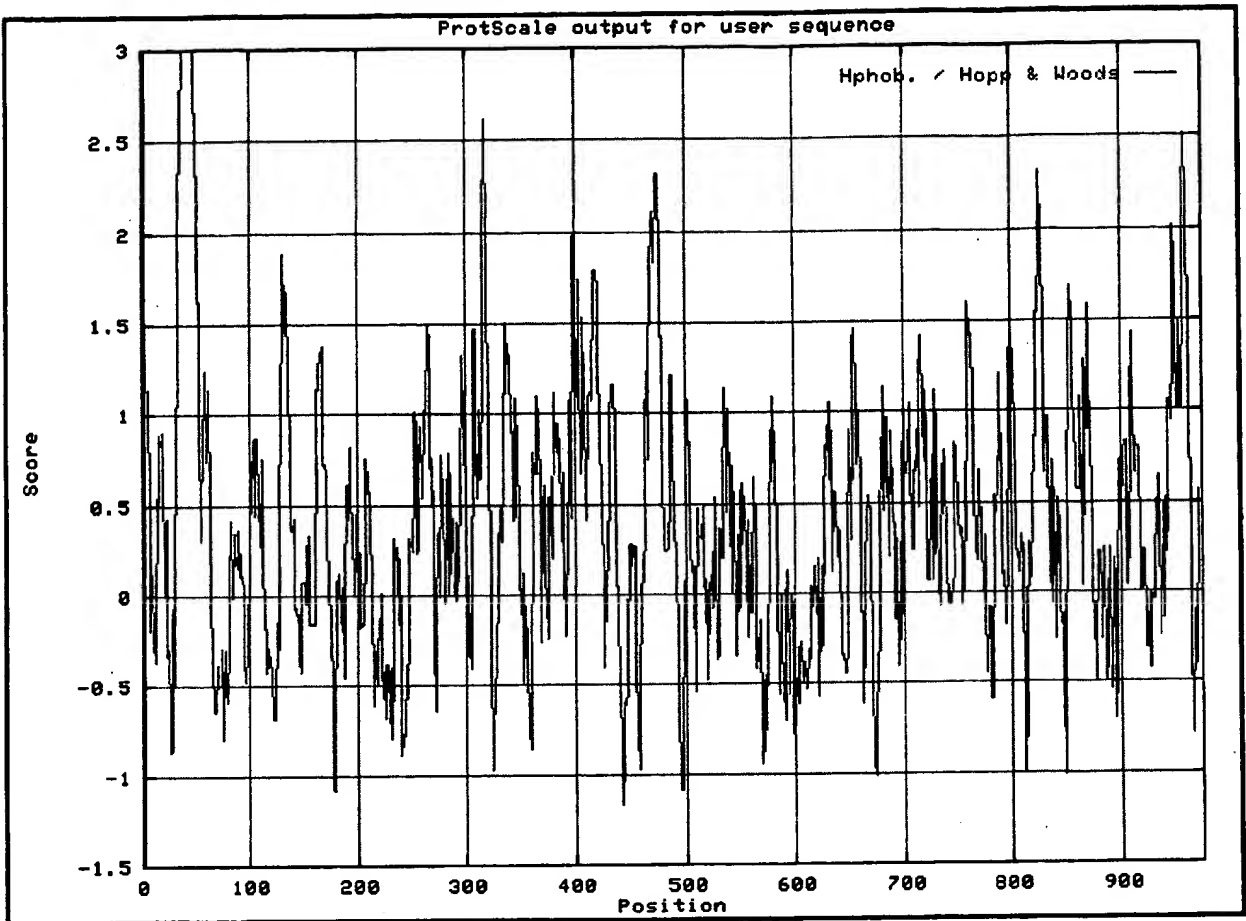
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.171

MAX: 3.000

1 - 974 of  
SEQ ID NO. 2  
(Chain 13)  
(22)



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## ProtScale

User-provided sequence:

```
      1      11      21      31      41      51
      |      |      |      |      |      |
1  MEDLDQSPLV SSSDSPPRPQ PAFKYQFVRE PEDEEEEEEE EEEDEDEDLE ELEVLERKPA  60
61 AGLSAAPVPT APAAGAPLMD FGNDVFPPAP RGPLPAAPPV APERQPSWDP SPVSSTVPAP  120
121 SPLSAAAVSP S
```

SEQUENCE LENGTH: 131

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

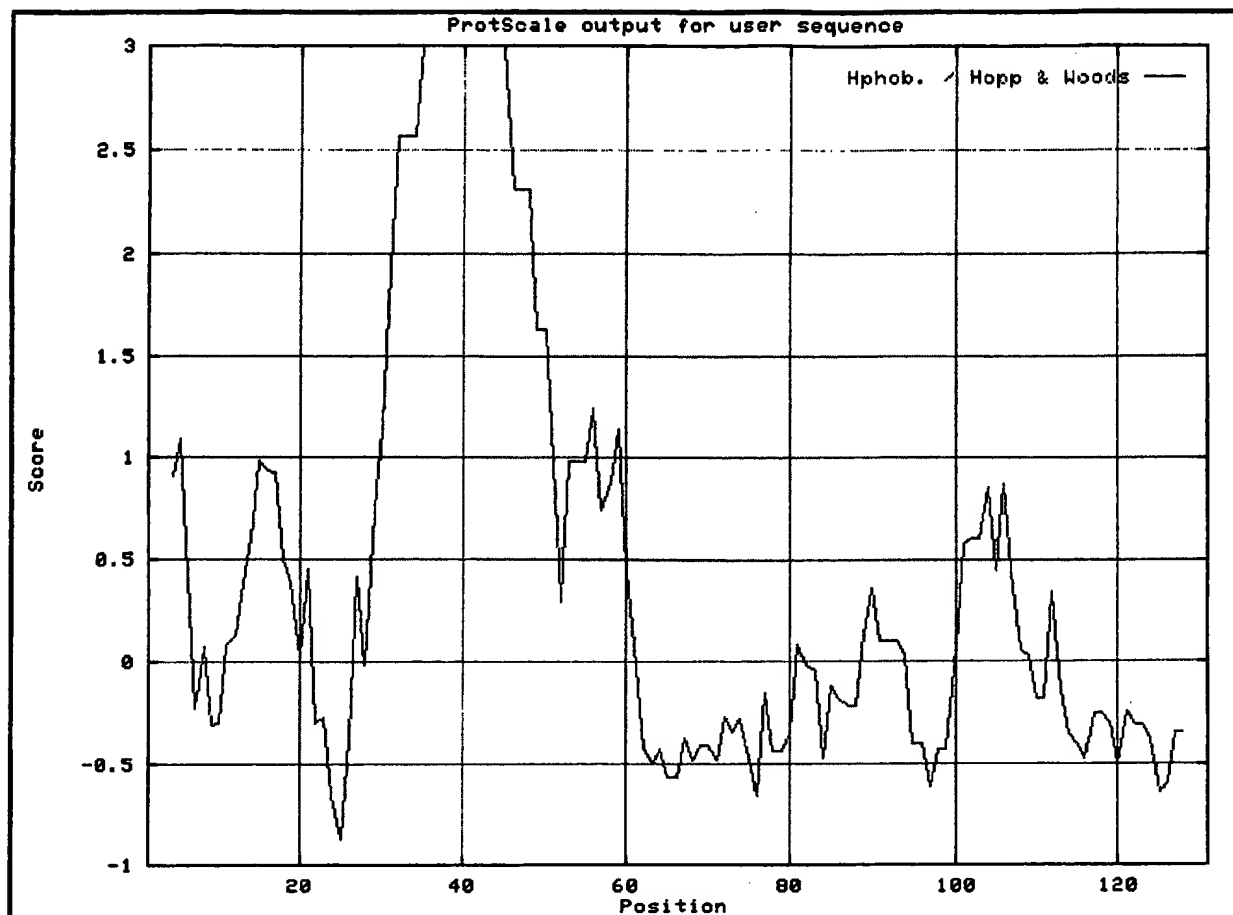
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -0.871

MAX: 3.000

1-131 of  
SEQ ID No. 29  
(c(13))<sup>(24)</sup>



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# ProtScale

User-provided sequence:

	1	11	21	31	41	51	
1	KLPEDDEPPA	RPPPPPPASV	SPQAEPVWTP	PAPAPAAPPS	TPAAPKRRGS	SGAVVXXXXK	60
61	IMDLKEQPGN	TISAGQEDFP	SVLLETAASX	PSLSPLSAAS	FKEHEYLGNL	STVLPTEGTL	120
121	QENVSEASKE	VSEKAKTLLI	DRDLTEFSEL	EYSEMGSSFS	VSPKAESAVI	VANPREEIIV	180
181	KNKDEEEKLV	SNNILHXQQE	LPTALTKLVK	EDEVVSSEKA	KDSFNEKRVA	VEAPMREEYA	240
241	DFKPFERVWE	VKDSKEDSDM	LAAGGKIESN	LESKVDKKCF	ADSLEQTNHE	KDSESSNDDT	300
301	SFPSTPEGIK	DRSGAYITCA	PFNPAATESI	ATNIFLLED	PTSENXTDEK	KIEEKKAQIV	360
361	TEKNTSTKTS	NPFFVAAQDS	ETDYVTTDNL	TKVTEEVVAN	MPEGLTPDLV	QEACESELNE	420
421	VTGTKIAYET	KMDLVQTSEV	MQESLYPAAQ	LCPSFEESEA	TPSPVLPDIV	MEAPLNSAVP	480
481	SAGASVIQPS	SSPLEASSVN	YESIKHEPEN	PPPYEEAMSV	SLKVSGIKEE	IKEPENINAA	540
541	LQETEAPYIS	IACDLIKETK	LSAEPAPDFS	DYSEMAKVEQ	PVPDHSELVE	DSSPDSEPVD	600
601	LFSDDSIPDV	PQKQDETVM	VKESLTETSF	ESMIEYENKE	KLSALPPEGG	KPYLESFKLS	660
661	LDNTKDTLLP	DEVSTLSKKE	KIPLQMEELS	TAVYSNDDLF	ISKEAQIRET	ETFSDDSSPIE	720
721	IIDEFPTLIS	SKTDSFSKLA	REYTDLEVSH	KSEIANAPDG	AGSLPCTELP	HDLCLKNIQP	780
781	KVEEKISFSD	DFSKNGSATS	KVLLLPDP				

SEQUENCE LENGTH: 808

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,...,7, using **linear weight variation model**:

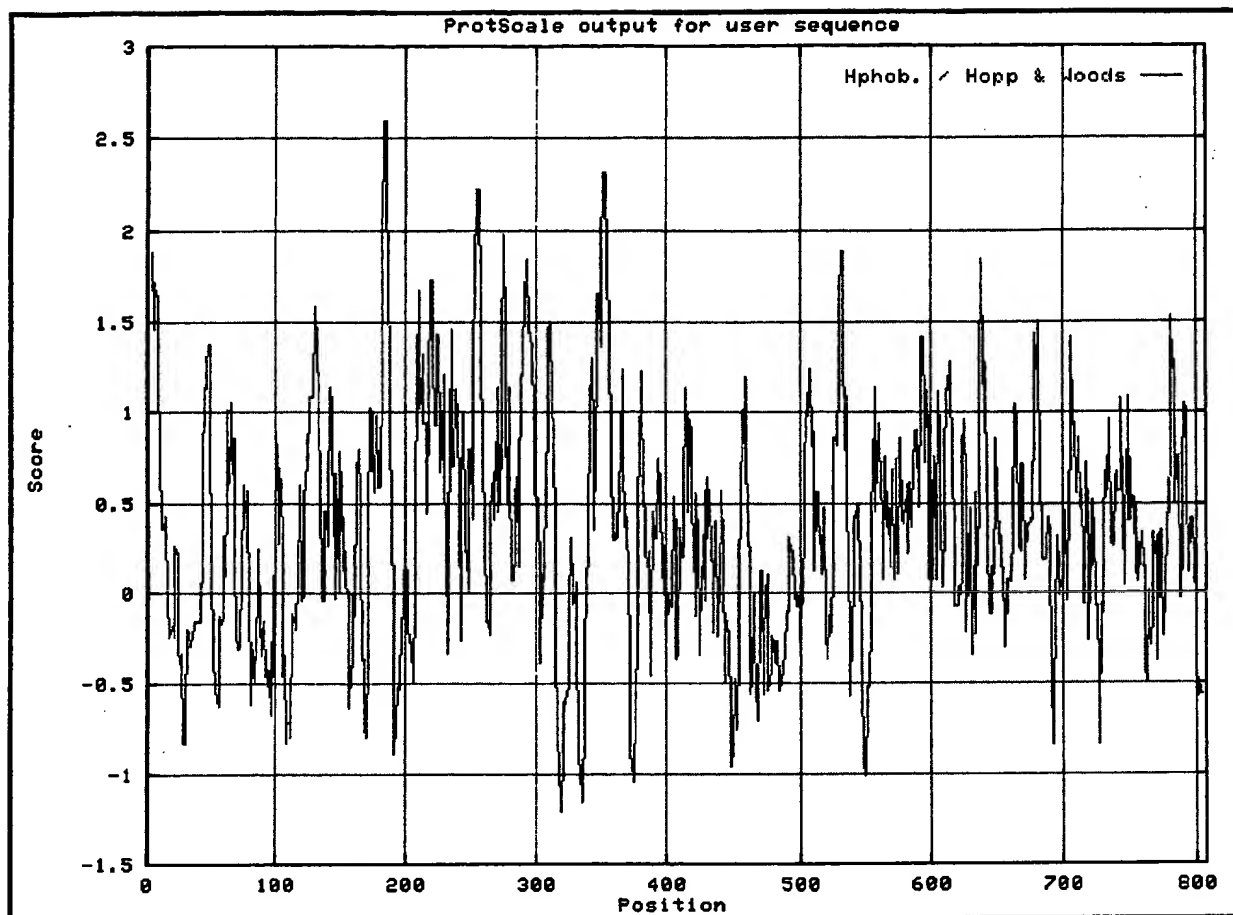
1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.214

MAX: 2.600

132-939 of  
SEQ ID No. 29  
(claim 13) (25)





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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	GOEDFPSVLL	ETAASXPSSL	PLSAASFKEH	EYLGNLSTVL	PTEGTLQENV	SEASKEVSEK 60
61	AKTLLIDRDL	TEFSELEYSE	MGSSFVSVPK	AESAVIVANP	REEIIVKNKD	EEKLVSNNI 120
121	LHXQQELPTA	LTKLVKEDEV	VSSEKAKDSF	NEKRVAVEAP	MREEYADFKP	FERVWEVKDS 180
181	KEDSDMLAAG	GKIESNLESK	VDKKCFADSL	EQTNHEKDSE	SSNDDTSFPS	TPEGIKDRSG 240
241	AYITCAPFNP	AATESIATNI	FPLLEDPTSE	NXTDEKKIEE	KKAQIVTEKN	TSTKTS

SEQUENCE LENGTH: 296

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

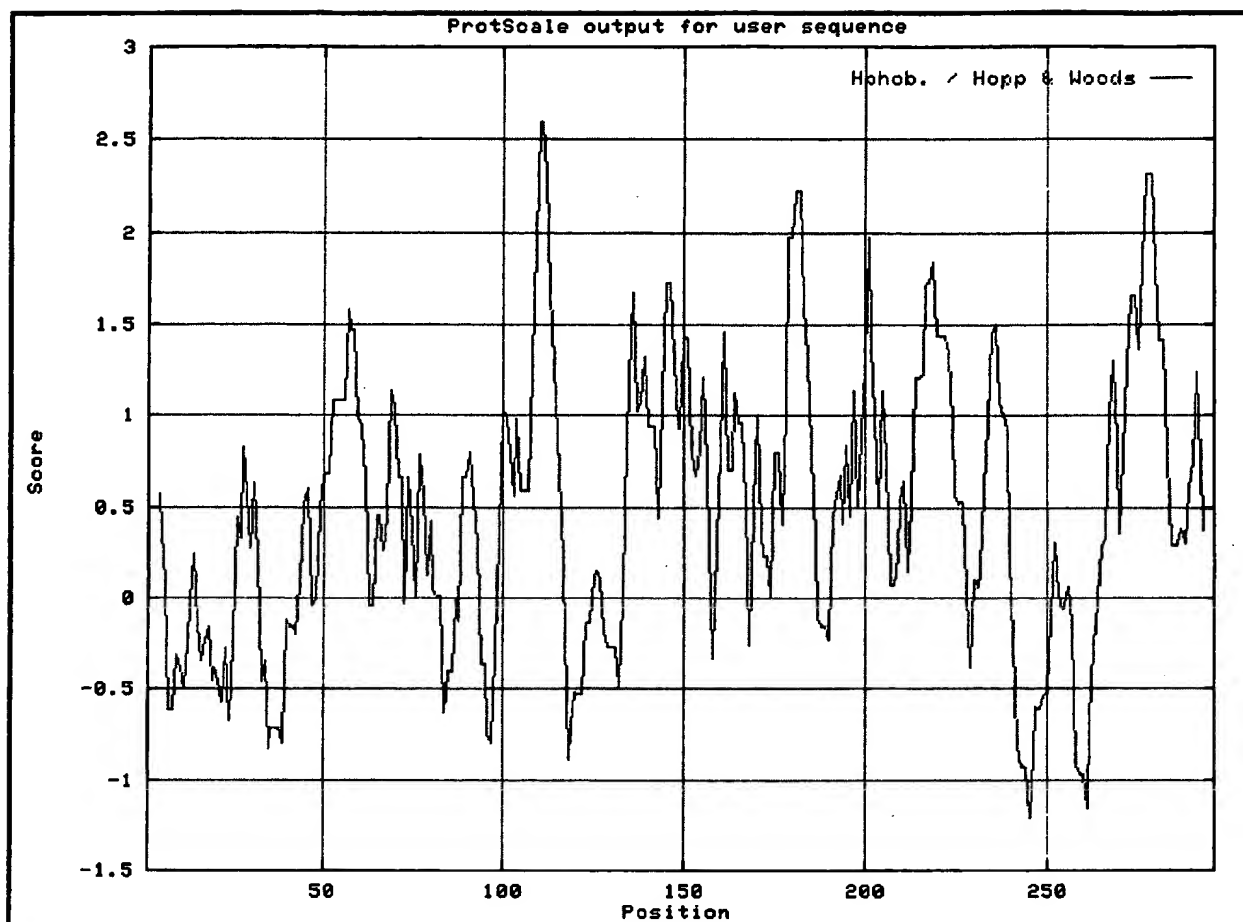
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.214

MAX: 2.600

206-501 of  
SEQ ID No. 29  
(claim 13) (26)



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# ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	SNPFFVAAQD	SETDYVTTDN	LTKVTEEVVA	NMPEGLTPDL	VQEACESELN	EVTGTKIAYE 60
61	TKMDLVQTSE	VMQESLYPAA	QLCPSFEESE	ATPSPVLPDI	VMEAPLNSAV	PSAGASVIQP 120
121	SSSPLEASSV	NYESIKHEPE	NPPPYEEAMS	VSLKVSGIKE	EIKEPENINA	ALQETEAPYI

SEQUENCE LENGTH: 180

Using the scale Hphob. / Hopp & Woods, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

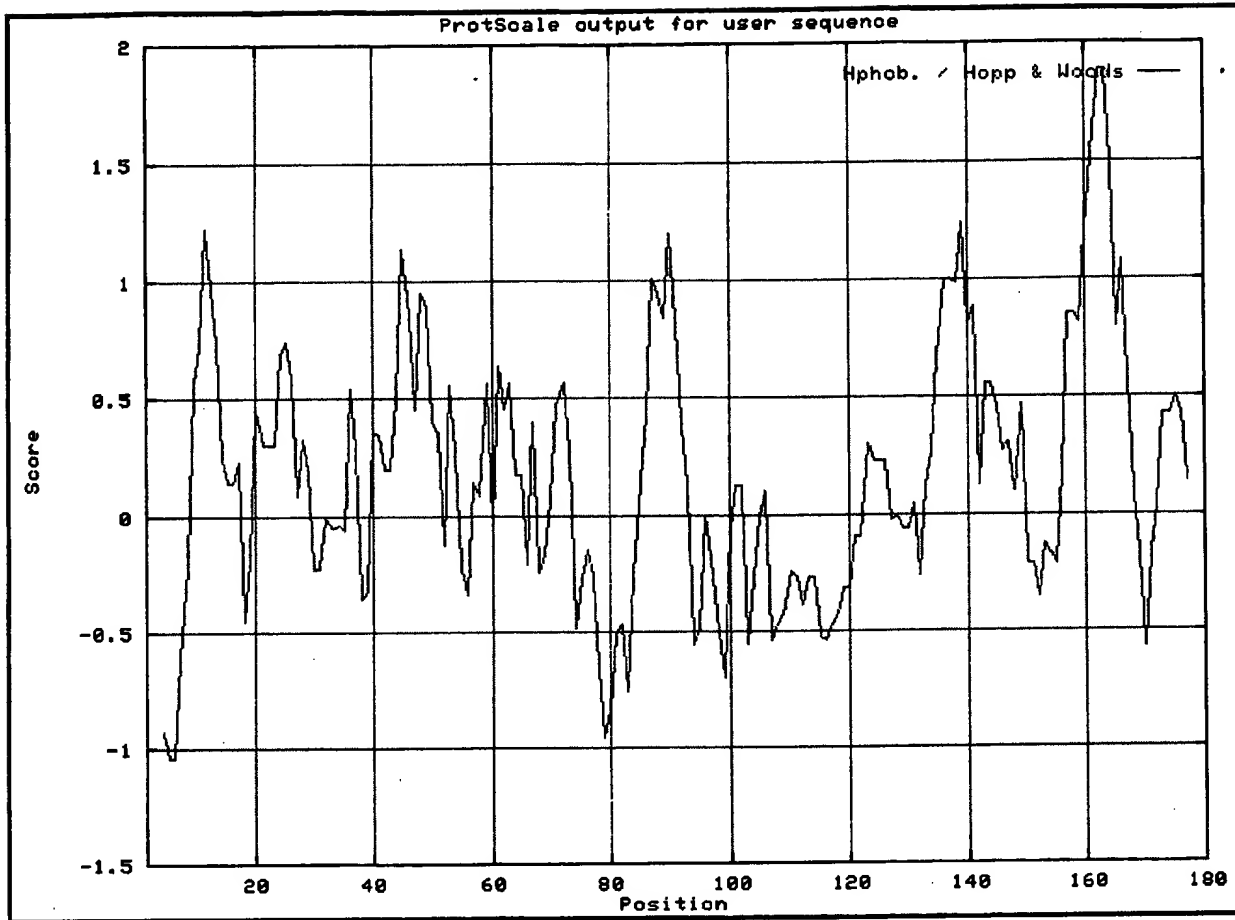
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.043

MAX: 1.886

501 - 680 of  
SEA ID No 29  
(chain 13) (27)



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# ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	VAPERQPSWD	PSPVSSTVPA	PSPLSAAAVS	PSKLPEDDEP	PARPPPPPPA	SVSPQAEPVW 60
61	TPPAPAPAAP	PSTPAAPKRR	GSSGAVVXXX	XKIMDLKEQP	GNTISAGQED	FPSVLLETAA 120
121	SXPSLSPLSA	ASFKEHEYL	GLSTVLPTG	TLQENVSEAS	KEVSEKAKTL	LIDRDLTEFS 180
181	ELEYSEMGSS	FSVSPKAESA	V			

SEQUENCE LENGTH: 201

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

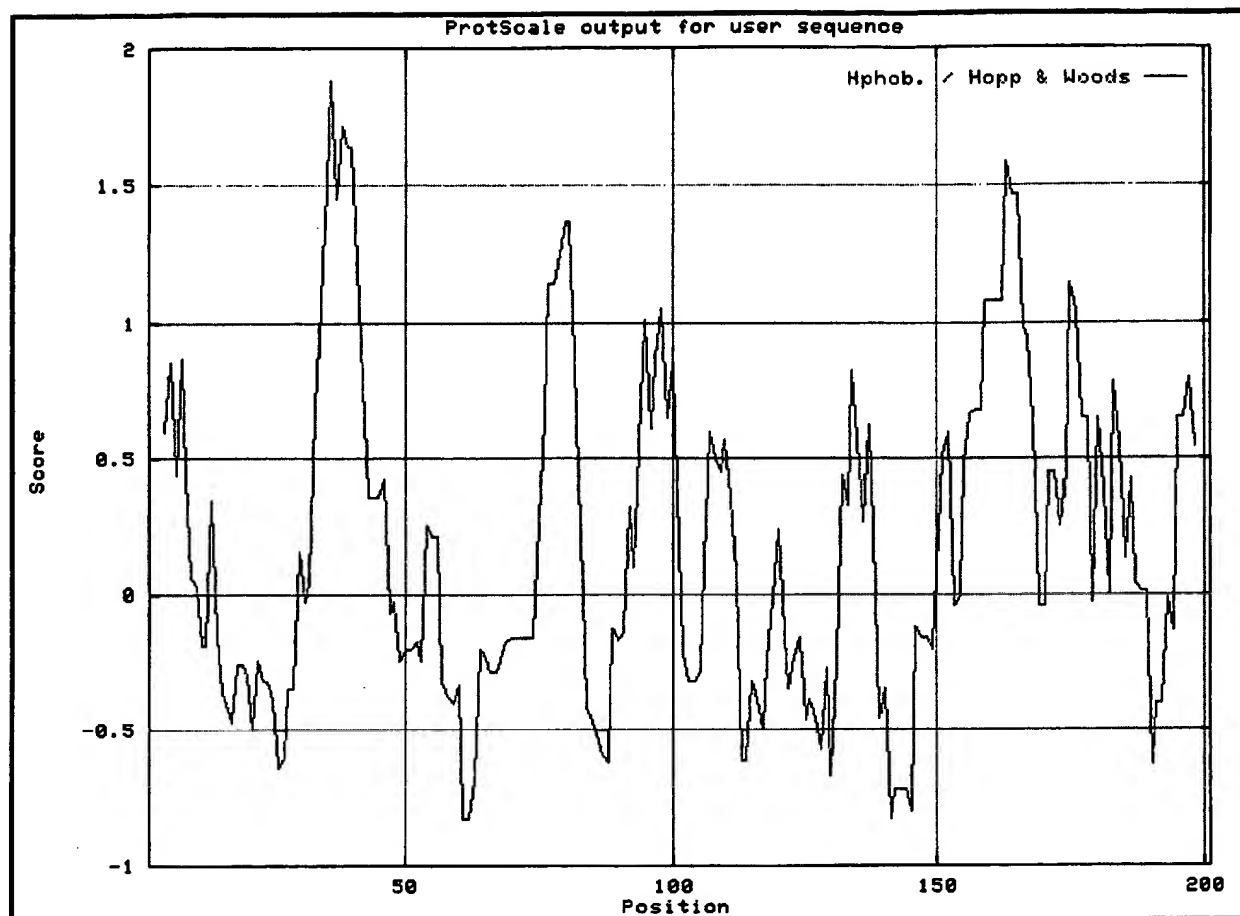
MIN: -0.829

MAX: 1.886

100-300 of  
Seq ID No 29  
(Clair 13)

132-206  
(32-106)

(28)



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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	ISIACDLIKE	TKLSAEPAPD	FSDYSEMAKV	EQVVPDHSEL	VEDSSPDSEP	VDLFSDD SIP 60
61	DVPQKQDETV	MLVKESLTET	SFESMIEYEN	KEKLSALPPE	GGKPYLESEFK	LSLDNTKDTL 120
121	LPDEVSTLSK	KEKIPLQMEE	LSTAVYSNDD	LFISKEAQIR	ETETFSDSSP	IEIIDEFPTL 180
181	ISSKTDSFSK	LAREYTDLEV	SHKSEIANAP	DGAGSLPCTE	LPHDLSLKNI	QPKVEEKISF 240
241	SDDFSKNGSA	TSKVLLLPD				

SEQUENCE LENGTH: 260

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,...,7, using linear weight variation model:

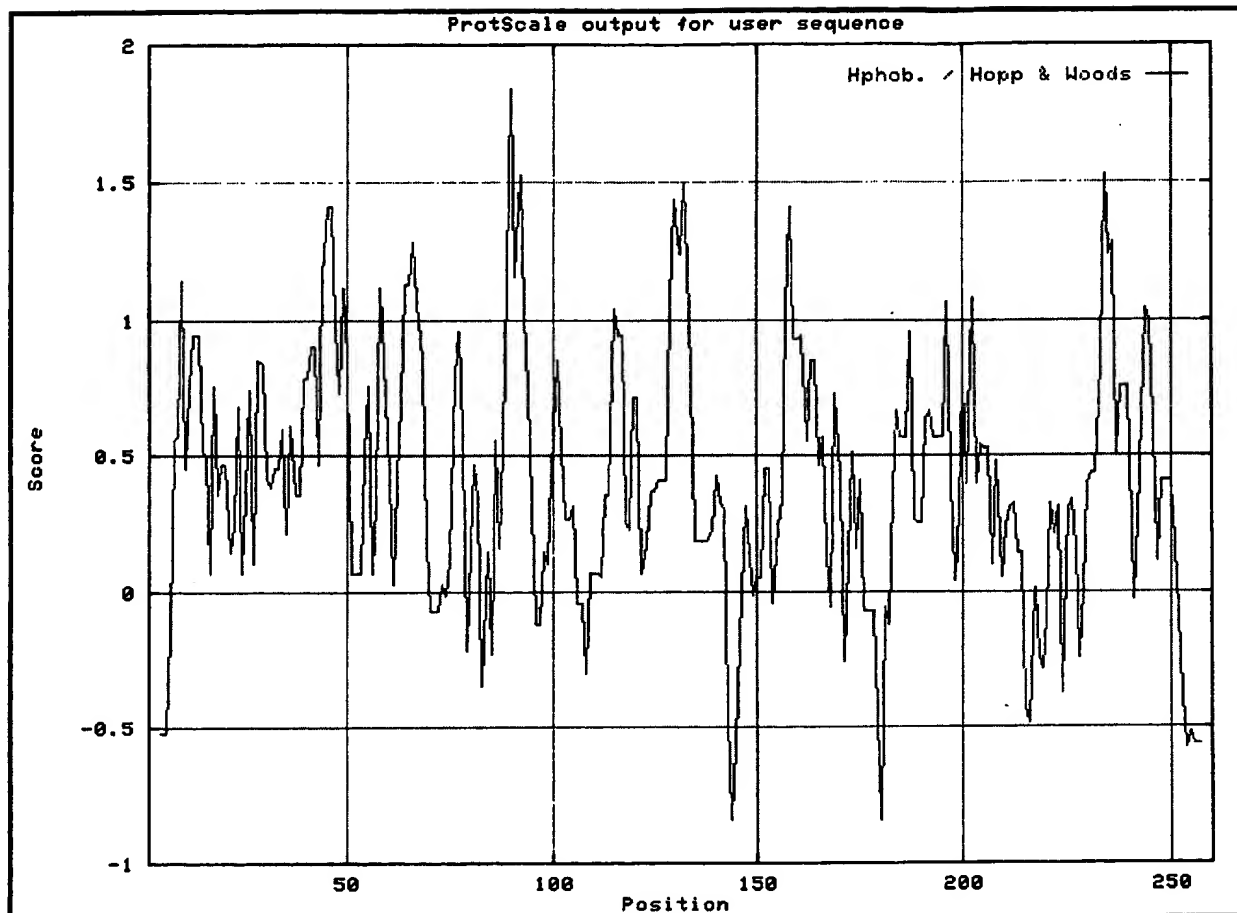
1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -0.843

MAX: 1.843

680-939 of  
SEQ ID No. 29  
(Claim 13) (29)





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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	VSALGHTQAE	IESIVKPKVL	EKEAEKKLPS	DTEKEDRSPS	AIFSADLGKT	SVVDLLYWRD 60
61	IKKTGVVFGA	SLFLLSLTV	FSIVSVTAYI	ALALLSVTIS	FRIYKGVIQA	IQSDEGHPP 120
121	RAYLESEVAI	SEELVQKYSN	SALGHVNCTI	KELRRLFLVD	DLVDSLKFAV	LMWVETYVGA 180
181	LFENGLTLL					

SEQUENCE LENGTH: 188

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

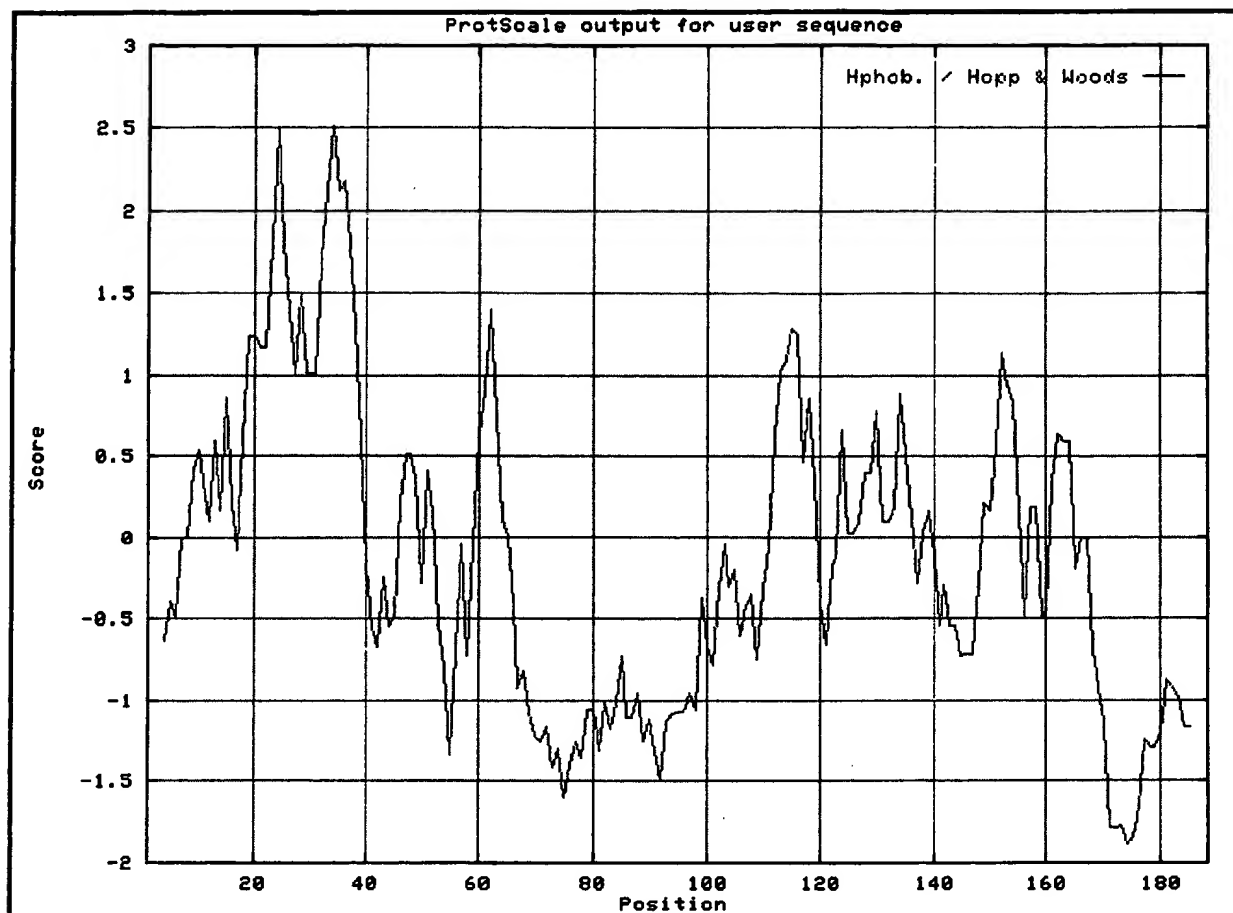
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.886

MAX: 2.514

940-1127 of  
SEQ ID No 29  
(claim 13) (33)



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## ProtScale

User-provided sequence:

1	11	21	31	41	51	
1	YETKVDLVQT	SEAIQESLYP	TAQLCPSFEE	AEATPSPVLP	DIVMEAPLNS	LLPSAGASVV 60
61	QPSVSPLEAP	PPVSYSIKL	EPENPPPYEE	AMNVALKALG	TKEGIKESPE	FNAAVQETEA 120
121	PYISIACDLI	KETKLSTEPS	PDFSNYSEIA	KFEKSVPEHA	ELVEDSSPES	EPVDLFSDDS 180
181	IPEVPQTQEE	AVMLMKESLT	E			

SEQUENCE LENGTH: 201

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

Weights for window positions 1,...,7, using **linear weight variation model**:

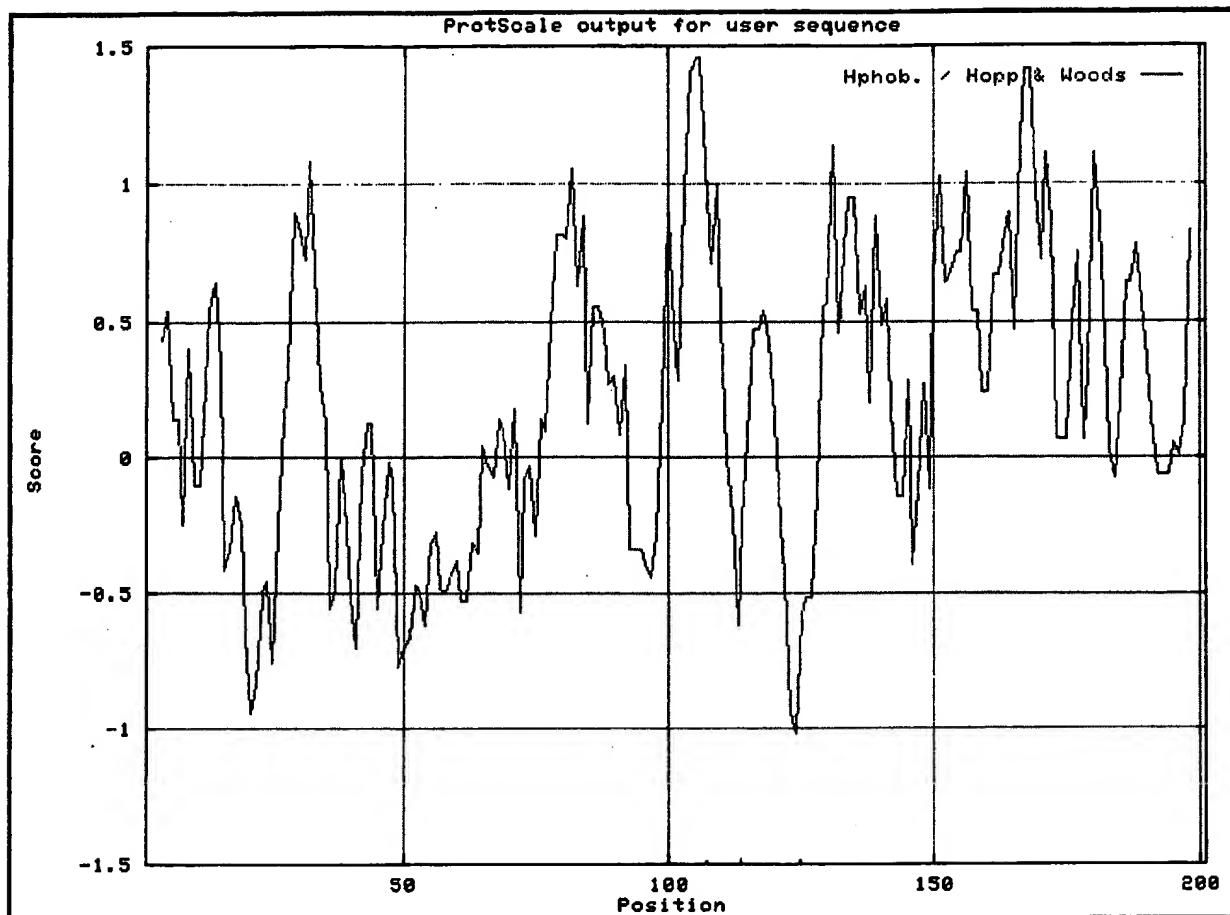
1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.014

MAX: 1.457

Clavin 18  
550-750 of  
Seq ID No. 2

623-640  
(73-90) (35)



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# ProtScale

## User-provided sequence:

```

      10      20      30      40      50      60
MEDLDQSPLV SSSDSPRPQ PAFKYQFVRE PEDEEEEEEE EEEDEDEDLE ELEVLERKPA
      70      80      90     100     110     120
AGLSAAPVPT APAAGAPLMD FGND FVPPAP RGPLPAAPPV APERQPSWDP SPVSSTVPAP
     130     140     150     160     170     180
SPLSAAAVSP SKLPEDDEPP ARPPPPPPAS VSPQAEPVWT PPAPAPAAPP STPAAPKRRG
     190     200
SSGAVVXXXX KIMDLKEQPG
SEQUENCE LENGTH: 200
```

---

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

---

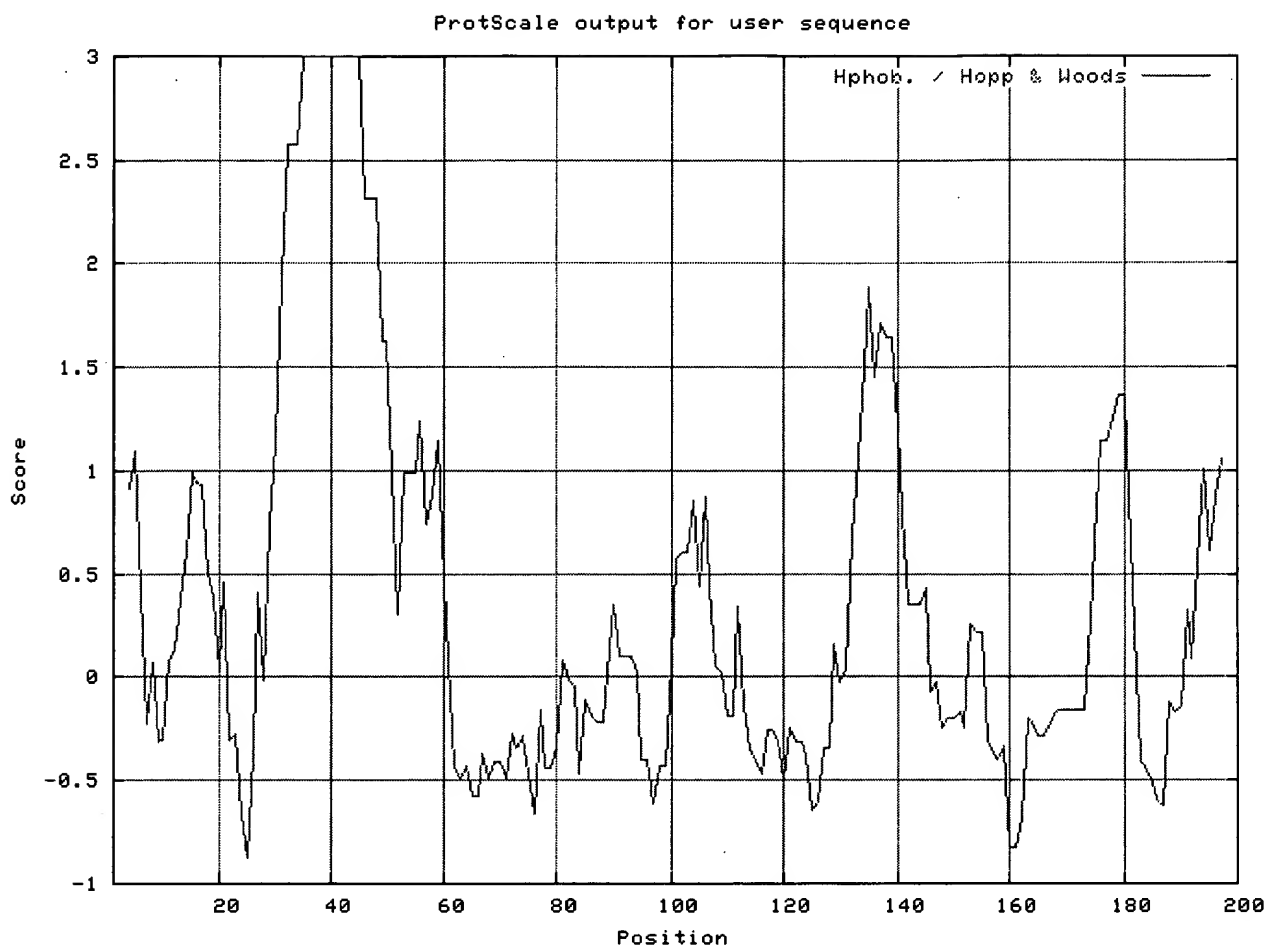
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

---

MIN: -0.871

MAX: 3.000



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# ProtScale

## User-provided sequence:

```

      10      20      30      40      50      60
VAPERQPSWD PSPVSSTVPA PSPLSAAAVS PSKLPEDDEP PARPPPPPPA SVSPQAEPVW
      70      80      90     100     110     120
TPPAPAPAAP PSTPAAPKRR GSSGAVVXXX XKIMDLKEQP GNTISAGQED FPSVLLETAA
     130     140     150     160     170     180
SXPSLSPLSA ASFKEHEYLG NLSTVLPTEG TLQENVSEAS KEVSEKAKTL LIDRDLTEFS
     190     200
ELEYSEMGSS FSVSPKAESA V
SEQUENCE LENGTH: 201

```

---

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

---

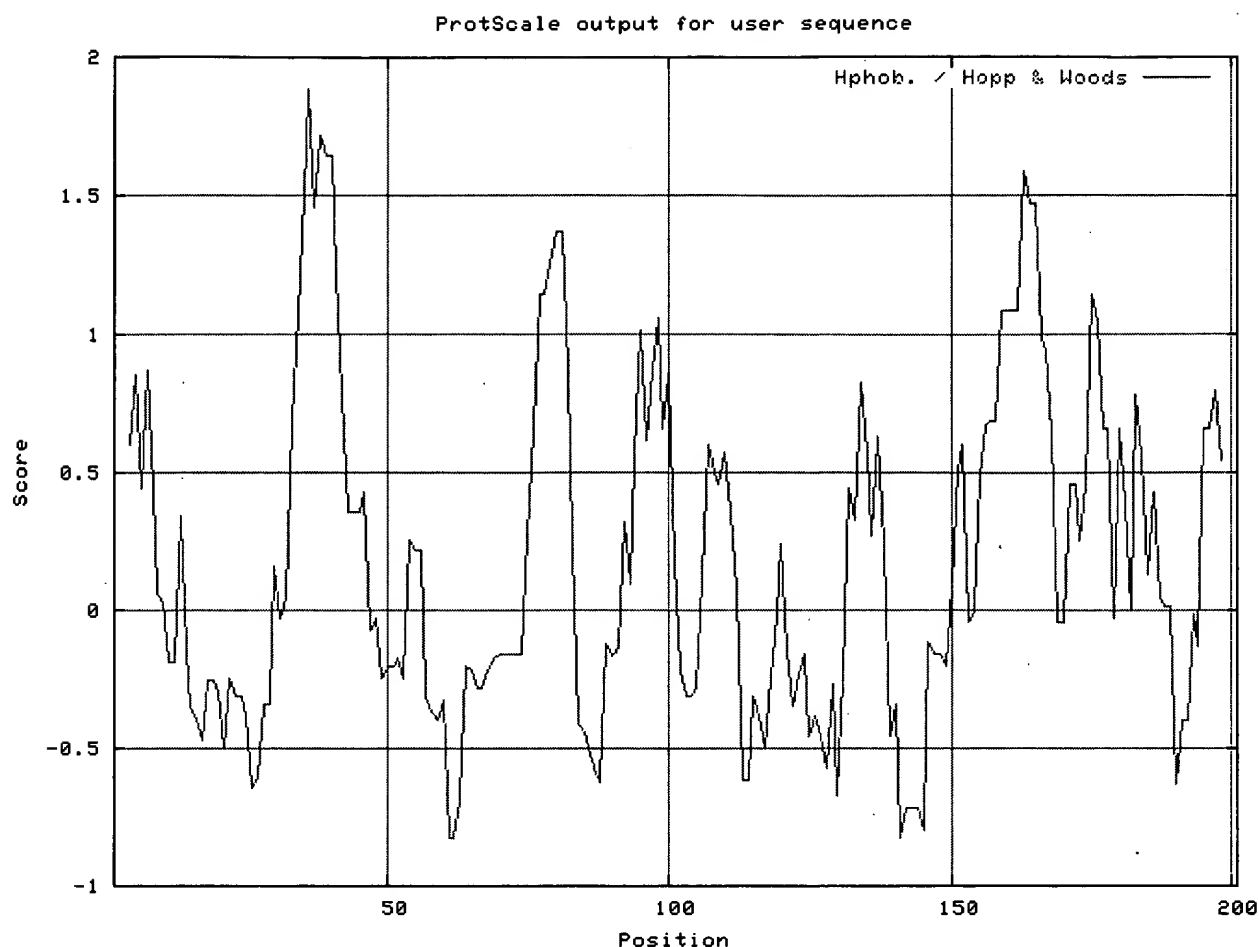
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

---

MIN: -0.829  
MAX: 1.886





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# ProtScale

## User-provided sequence:

```

      10      20      30      40      50      60
TLQENVSEAS KEVSEKAKTL LIDRDLTEFS ELEYSEMGSS FSVSPKAESA VIVANPREEI
      70      80      90     100     110     120
IVKNKDEEEK LVSNNILHXQ QELPTALTKL VKEDEVVSSE KAKDSFNEKR VAVEAPMREE
     130     140     150     160     170     180
YADFKPFERV WEVKDSKEDS DMLAAGGKIE SNLESKVDKK CFADSLEQTN HEKDSESSND
     190     200
DTSFPSTPEG IKDRSGAYIT C
SEQUENCE LENGTH: 201

```

---

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

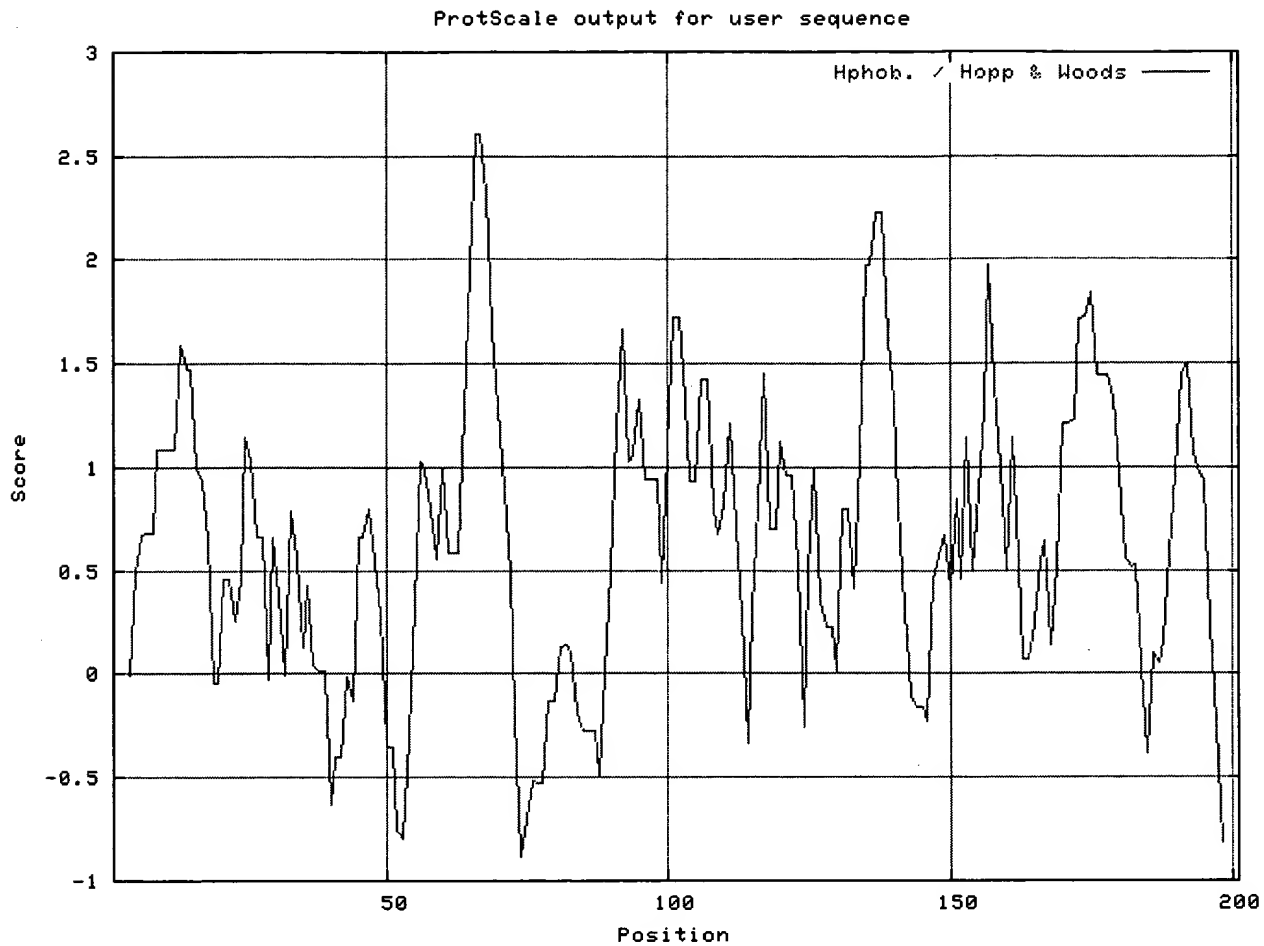
---

Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

---

MIN: -0.886  
 MAX: 2.600



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# ProtScale

## User-provided sequence:

10 20 30 40 50  
EVMQESLYPA AQLCPSFEES EATPSPVLPD IVMEAPLNSA VPSAGASVIQ  
SEQUENCE LENGTH: 50

---

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala:	-0.500	Arg:	3.000	Asn:	0.200	Asp:	3.000	Cys:	-1.000	Gln:	0.200
Glu:	3.000	Gly:	0.000	His:	-0.500	Ile:	-1.800	Leu:	-1.800	Lys:	3.000
Met:	-1.300	Phe:	-2.500	Pro:	0.000	Ser:	0.300	Thr:	-0.400	Trp:	-3.400
Tyr:	-2.300	Val:	-1.500	Asx:	1.600	Glx:	1.600	Xaa:	-0.215		

---

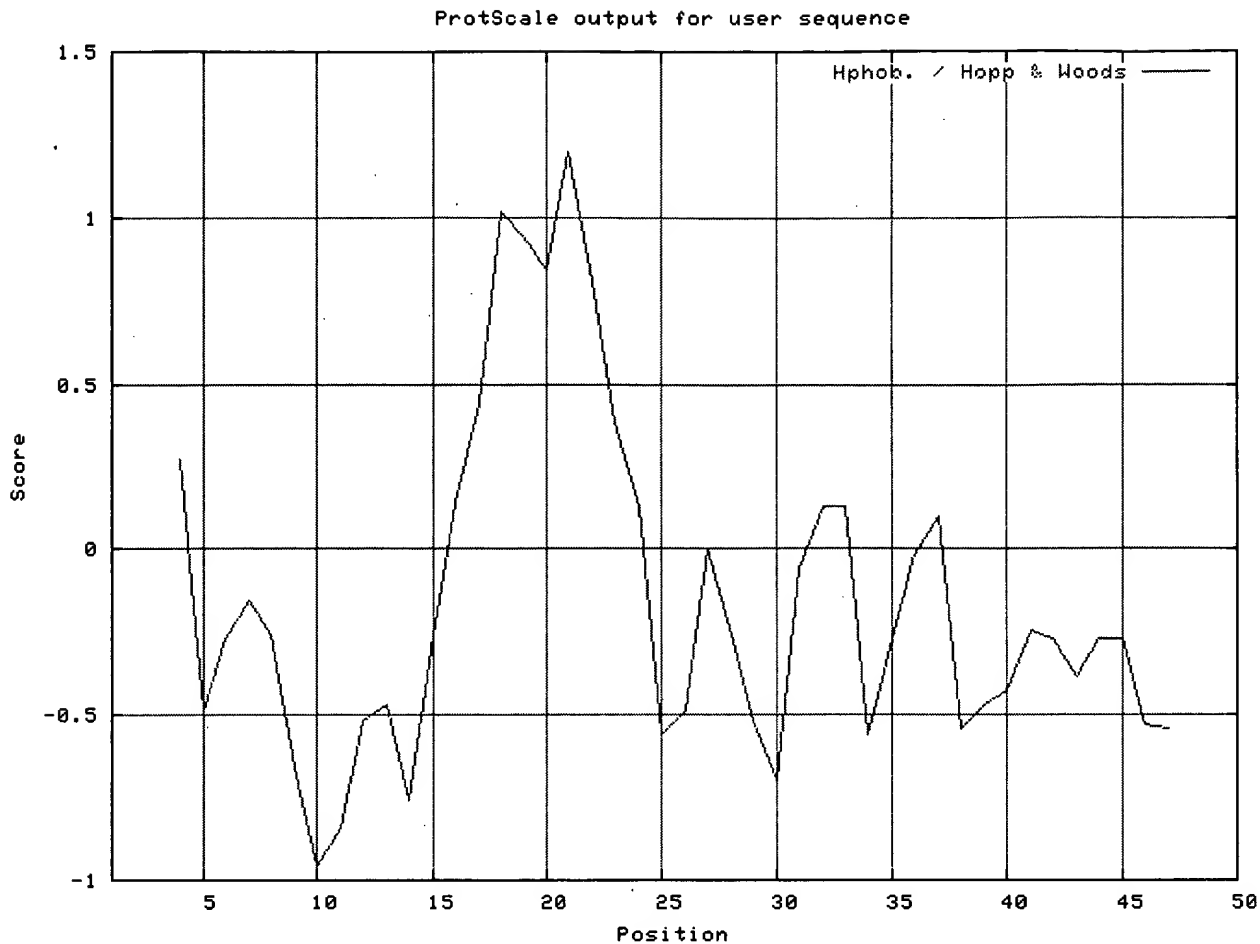
Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

---

MIN: -0.957

MAX: 1.200



The results of your ProtScale query are available in the following formats:

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# ProtScale

## User-provided sequence:

```

      10      20      30      40      50      60
RLSASPQELG KPYLESFQPN LHSTKDAASN DIPTLTKEK ISLQMEEFNT AIYSNDDLLS
      70      80      90     100     110     120
SKEDKIKESE TFSOSSPIEI IDEFPFVSA KDDSPKLAKE YTDLEVSDKS EIANIQSGAD
     130     140     150     160     170     180
SLPCLELPCD LSFKNIPKD EVHVSDEFSE NRSSVSKASI SPSNVSALEP QTEMGSIKVS
     190     200     210     220     230     240
KSLTKEAEKK LPSDTEKEDR SLSAVLSAEL SKTSVVDLLY WRDIKKTGVV FGASLFLLLS
     250     260     270     280     290     300
LTVFSIVSVT AYIALALLSV TISFRIYKGV IQAIQKSDEG HPFRAYLESE VAISEELVQK
     310     320     330     340     350     360
YSNSALGHVN STIKELRRLF LVDDLVDLKL FAVLMWVFTY VGALFNGLTL LILALISLFS
     370     380     390     400
IPVIYERHQQ QIDHYLGLAN KSVKDAMAKI QAKIPGLKRR AD
SEQUENCE LENGTH: 402

```

---

Using the scale **Hphob. / Hopp & Woods**, the individual values for the 20 amino acids are:

Ala: -0.500	Arg: 3.000	Asn: 0.200	Asp: 3.000	Cys: -1.000	Gln: 0.200
Glu: 3.000	Gly: 0.000	His: -0.500	Ile: -1.800	Leu: -1.800	Lys: 3.000
Met: -1.300	Phe: -2.500	Pro: 0.000	Ser: 0.300	Thr: -0.400	Trp: -3.400
Tyr: -2.300	Val: -1.500	Asx: 1.600	Glx: 1.600	Xaa: -0.215	

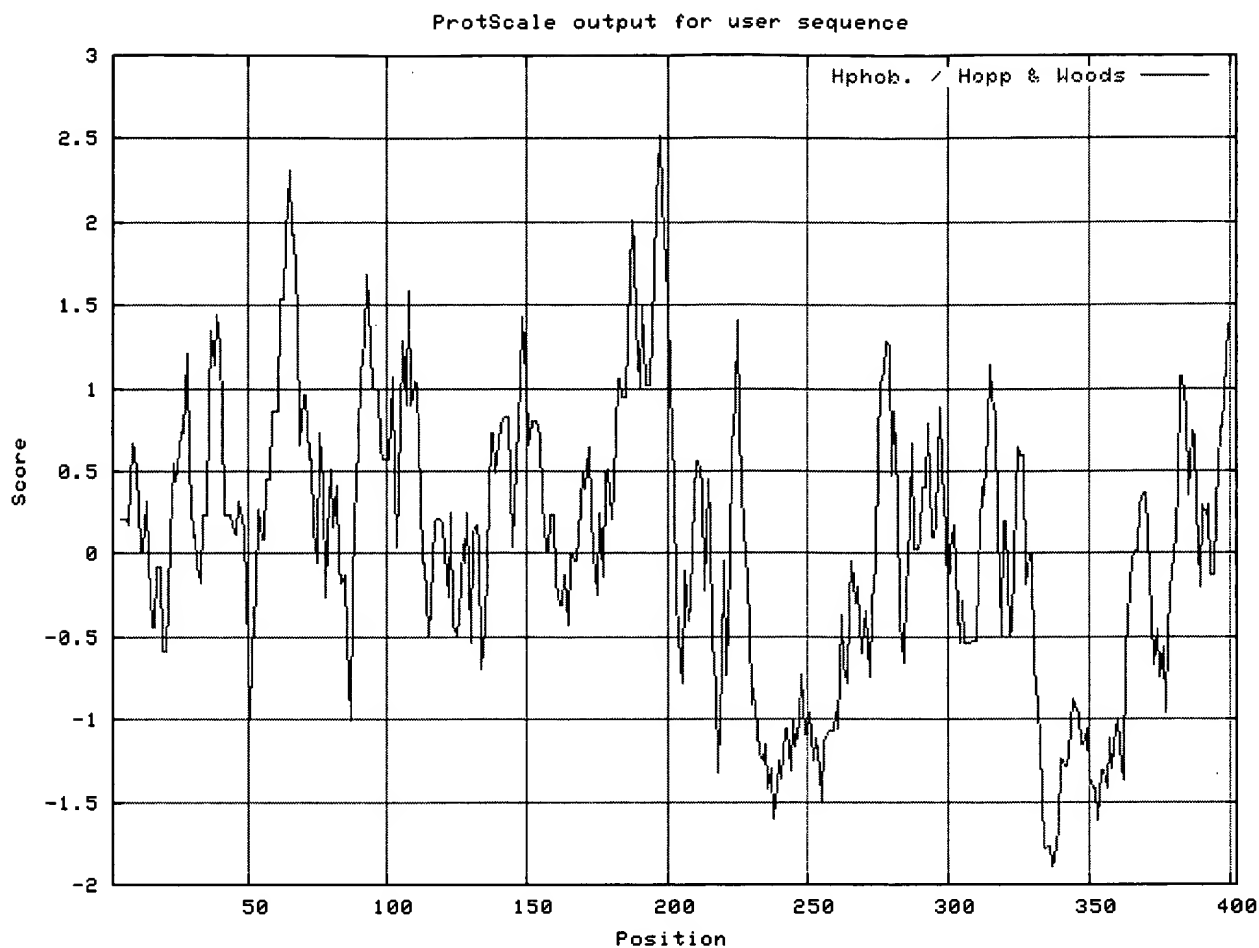
---

Weights for window positions 1,...,7, using **linear weight variation model**:

1	2	3	4	5	6	7
1.00	1.00	1.00	1.00	1.00	1.00	1.00
edge			center			edge

MIN: -1.886

MAX: 2.514



The results of your ProtScale query are available in the following formats:

- Image in GIF-format
- Image in Postscript-format
- Numerical format (verbose)
- Numerical format (minimal, to be exported into an external application)

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